

SEQUENCE LISTING

<110> Chapman, Edwin R.
Dong, Min

<120> BOTULINUM NEUROTOXIN B RECEPTORS AND USE THEREOF

<130> 960296.99004

<150> 60/422,951
<151> 2002-10-31

<150> 60/498,128
<151> 2003-08-27

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<170> PatentIn version 3.2

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Val Pro His Asn Ala Thr Glu Pro Ala Ser Pro Gly Glu Gly Lys Glu			
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Leu Leu Val Val Thr Cys Cys Phe Cys Val Cys Lys Lys Cys Leu Phe			
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Ile Asn Met Lys Asp Val Lys Asp Leu Gly Lys Thr Met Lys Asp Gln			
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Gln Phe Thr Phe Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu
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Gly Glu Phe Lys Val Pro Met Asn Thr Val Asp Phe Gly His Val Thr
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Ser His Pro Glu Ala	Leu Ala Ala	Pro Val Thr	Thr Val Ala	Thr Leu		
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Tyr	Asp	Phe	Asp	Arg	Phe	Ser	Lys	His	Asp	Ile	Ile	Gly	Glu	Phe	Lys	
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Gly Ile Ile Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr
165 170 175

Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Glu Lys Lys Lys Lys
180 185 190

Phe Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Val Phe Asn Glu
195 200 205

Gln Phe Thr Phe Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu
210 215 220

Val Met Ala Val Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile
225 230 235 240

Gly Glu Phe Lys Val Pro Met Asn Thr Val Asp Phe Gly His Val Thr
245 250 255

Glu Glu Trp Arg Asp Leu Gln Ser Ala Glu Lys Glu Glu Gln Glu Lys
260 265 270

Leu Gly Asp Ile Cys Phe Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys
275 280 285

Leu Thr Val Val Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val
290 295 300

Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn Gly
305 310 315 320

Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile Lys Lys Asn Thr Leu Asn
325 330 335

Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu Val Pro Phe Glu Gln Ile
340 345 350

Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Ile Gly
355 360 365

Lys Asn Asp Ala Ile Asp Lys Val Phe Val Gly Tyr Asn Ser Thr Gly
370 375 380

Ala Glu Leu Arg His Trp Ser Asp Ile Leu Ala Asn Pro Arg Arg Pro
385 390 395 400

Ile Ala Gln Trp His Thr Leu Gln Val Glu Glu Glu Val Asp Ala Met
405 410 415

Leu Ala Val Lys Lys
420

<210> 5
<211> 422
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

<222> (33)..(53)
<223> BoNT/B binding domain

<220>
<221> MISC_FEATURE
<222> (54)..(80)
<223> Gangliosides binding domain or transmembrane domain

<400> 5

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Thr Val Ala Thr Val Leu Pro Ser Asn Ala Thr Glu Pro Ala Ser Pro
20 25 30

Gly Glu Gly Lys Glu Asp Ala Phe Ser Lys Leu Lys Glu Lys Phe Met
35 40 45

Asn Glu Leu His Lys Ile Pro Leu Pro Pro Trp Ala Leu Ile Ala Ile
50 55 60

Ala Ile Val Ala Val Leu Leu Val Leu Thr Cys Cys Phe Cys Ile Cys
65 70 75 80

Lys Lys Cys Leu Phe Lys Lys Asn Lys Lys Lys Gly Lys Glu Lys
85 90 95

Gly Gly Lys Asn Ala Ile Asn Met Lys Asp Val Lys Asp Leu Gly Lys
100 105 110

Thr Met Lys Asp Gln Ala Leu Lys Asp Asp Asp Ala Glu Thr Gly Leu
115 120 125

Thr Asp Gly Glu Glu Lys Glu Glu Pro Lys Glu Glu Lys Leu Gly
130 135 140

Lys Leu Gln Tyr Ser Leu Asp Tyr Asp Phe Gln Asn Asn Gln Leu Leu
145 150 155 160

Val Gly Ile Ile Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly
165 170 175

Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys
180 185 190

Lys Phe Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Val Phe Asn
195 200 205

Glu Gln Phe Thr Phe Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr
210 215 220

Leu Val Met Ala Val Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile
225 230 235 240

Ile Gly Glu Phe Lys Val Pro Met Asn Thr Val Asp Phe Gly His Val
245 250 255

Thr Glu Glu Trp Arg Asp Leu Gln Ser Ala Glu Lys Glu Glu Gln Glu
260 265 270

Lys Leu Gly Asp Ile Cys Phe Ser Leu Arg Tyr Val Pro Thr Ala Gly
275 280 285

Lys Leu Thr Val Val Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp
290 295 300

Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn
305 310 315 320

Gly Lys Arg Leu Lys Lys Lys Thr Thr Ile Lys Lys Asn Thr Leu
325 330 335

Asn Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu Val Pro Phe Glu Gln
340 345 350

Ile Gln Lys Val Gln Val Val Thr Val Leu Asp Tyr Asp Lys Ile
355 360 365

Gly Lys Asn Asp Ala Ile Gly Lys Val Phe Val Gly Tyr Asn Ser Thr
370 375 380

Gly Ala Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg
385 390 395 400

Pro Ile Ala Gln Trp His Thr Leu Gln Val Glu Glu Glu Val Asp Ala
405 410 415

Met Leu Ala Val Lys Lys
420

<210> 6
<211> 1876
<212> DNA
<213> Mus musculus

<220>
 <221> CDS
 <222> (16)..(1284)

<220>
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 <222> (133)..(195)
 <223> BoNT/B binding domain

<220>
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 <222> (196)..(276)
 <223> Gangliosides binding domain or transmembrane domain

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		1				5						10			

gtg	gct	ccg	gcc	acc	acc	act	gcc	aca	atg	ccc	ctt	gca	ccc	gtc	gca	99
Val	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Thr	Met	Pro	Leu	Ala	Pro	Val	Ala	
15						20						25				

cct	gcc	gac	aac	tct	aca	gag	agc	acg	ggt	cct	ggg	gag	agc	caa	gaa	147
Pro	Ala	Asp	Asn	Ser	Thr	Glu	Ser	Thr	Gly	Pro	Gly	Glu	Ser	Gln	Glu	
30						35						40				

gac	atg	ttc	gcc	aag	ctg	aag	gag	aaa	ttc	ttc	aat	gag	atc	aac	aag	195
Asp	Met	Phe	Ala	Lys	Leu	Lys	Glu	Lys	Phe	Phe	Asn	Glu	Ile	Asn	Lys	
45					50					55			60			

atc	ccc	ttg	ccc	ccc	tgg	gct	ctg	atc	gcc	atg	gct	gtg	gtt	gct	ggc	243
Ile	Pro	Leu	Pro	Pro	Trp	Ala	Leu	Ile	Ala	Met	Ala	Val	Val	Ala	Gly	
65						70						75				

ctc	ctg	ctg	ctc	acc	tgt	tgc	ttc	tgc	atc	tgt	aag	aag	tgc	tgc	tgc	291
Leu	Leu	Leu	Leu	Thr	Cys	Cys	Phe	Cys	Ile	Cys	Lys	Lys	Cys	Cys	Cys	
80						85					90					

aag	aag	aag	aac	aag	aag	gag	aag	ggc	aaa	ggc	atg	aag	aac	gcc		339
Lys	Lys	Lys	Asn	Lys	Lys	Glu	Lys	Gly	Lys	Gly	Met	Lys	Asn	Ala		
95						100					105					

atg	aac	atg	aag	gac	atg	aaa	ggg	ggc	cag	gat	gac	gat	gat	gca	gag	387
Met	Asn	Met	Lys	Asp	Met	Lys	Gly	Gly	Gly	Gln	Asp	Asp	Asp	Ala	Glu	
110						115					120					

aca	ggc	ctg	act	gaa	gga	gaa	ggt	gaa	ggc	gag	gag	gag	aaa	gag	cca	435
Thr	Gly	Leu	Thr	Glu	Gly	Glu	Gly	Glu	Gly	Glu	Glu	Glu	Lys	Glu	Pro	
125					130					135			140			

gag	aac	ctg	ggc	aaa	ttg	cag	ttt	tct	ctg	gac	tat	gat	ttc	cag	gcc	483
Glu	Asn	Leu	Gly	Lys	Leu	Gln	Phe	Ser	Leu	Asp	Tyr	Asp	Phe	Gln	Ala	
145						150						155				

aac	cag	ctc	acc	gtg	ggt	gtc	ctg	cag	gct	gcg	gaa	ctc	cca	gcc	ctg	531
Asn	Gln	Leu	Thr	Val	Gly	Val	Leu	Gln	Ala	Ala	Glu	Leu	Pro	Ala	Leu	
160						165					170					

gac atg ggt ggc aca tca gac cct tat gtc aaa gtc ttc ctc ctc cca Asp Met Gly Gly Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro	579
175 180 185	
gac aag aag aag aaa tat gag act aag gtg cat cgg aag acg ctg aac Asp Lys Lys Lys Tyr Glu Thr Lys Val His Arg Lys Thr Leu Asn	627
190 195 200	
cca gcc ttc aat gag aca ttc act ttc aag gtg cca tac cag gag tta Pro Ala Phe Asn Glu Thr Phe Thr Phe Lys Val Pro Tyr Gln Glu Leu	675
205 210 215 220	
gca ggc aag acc ctg gtg atg gca atc tat gac ttt gac cgc ttc tct Ala Gly Lys Thr Leu Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser	723
225 230 235	
aag cat gac atc atc ggg gag gtg aag gta ccc atg aac aca gtg gac Lys His Asp Ile Ile Gly Glu Val Lys Val Pro Met Asn Thr Val Asp	771
240 245 250	
ctt ggc cag ccc atc gag gaa tgg aga gac cta caa ggc gga gag aag Leu Gly Gln Pro Ile Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys	819
255 260 265	
gaa gag cca gag aag ttg ggt gac atc tgt acc tcc ttg cgc tac gtg Glu Glu Pro Glu Lys Leu Gly Asp Ile Cys Thr Ser Leu Arg Tyr Val	867
270 275 280	
ccc aca gct ggg aag ctc acc gtc tgt atc ctg gag gcc aag aac ctg Pro Thr Ala Gly Lys Leu Thr Val Cys Ile Leu Glu Ala Lys Asn Leu	915
285 290 295 300	
aag aag atg gac gta ggg ggc ctt tca gac ccc tat gtg aag atc cac Lys Lys Met Asp Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His	963
305 310 315	
ctg atg cag aac ggt aag aga ctc aag aag aag acg aca gtg aag Leu Met Gln Asn Gly Lys Arg Leu Lys Lys Lys Thr Thr Val Lys	1011
320 325 330	
aag aag acc ctg aac ccc tac ttc aac gag tcc ttc agc ttc gag atc Lys Lys Thr Leu Asn Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile	1059
335 340 345	
ccc ttt gag cag atc cag aaa gtc cag gtg gtc gtc acc gtg cta gac Pro Phe Glu Gln Ile Gln Lys Val Gln Val Val Val Thr Val Leu Asp	1107
350 355 360	
tac gac aaa ctg ggc aag aat gaa gcc atc gga aag atc ttt gta ggc Tyr Asp Lys Leu Gly Lys Asn Glu Ala Ile Gly Lys Ile Phe Val Gly	1155
365 370 375 380	
agc aac gcc aca ggc acc gag ttg cgg cac tgg tcc gac atg ctg gcc Ser Asn Ala Thr Gly Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala	1203
385 390 395	
aac cct cggtt agg ccc att gcc cag tgg cac tct ctt aag cct gag gaa Asn Pro Arg Arg Pro Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu	1251
400 405 410	
gaa gtg gat gct ctt ctg ggc aag aac aag tag gctccagcggttccac	1304

Glu Val Asp Ala Leu Leu Gly Lys Asn Lys
415 420

gccccctaagg agccacgcggcc ccgaggcgcc acgccccctg aggacactga cgagatccag 1364
agctatatcaat acctcagtttta cgcgacctta gaggtttttt catttttttgc cggtgtgtcc 1424
tgtttttcct tcctttttct ctttttaaag accaacttcc ttttggtggc tttgtgtgaaga 1484
gagtcccccta agaggtgaaa gaaaaggctg gctctgttat tgccccggg gcggtccttg 1544
ttgcacatgcggcc ttacacgggtt tcccccttac cccaagtggg gcccctctact gtcagacagt 1604
tgaaggacta actgcttttc ctgggtttt gaccaacaac atggcaagca cattctgttt 1664
cttgactgtg aaggcaacat agtggccagc attgtgtgtg tgtgtgtgtg tgtgtgtgtg 1724
tatgtgtgtg tgtacacactg tatgtgccccca tccatccccca cctgcctgtt ttgaacatct 1784
ctcttcattt tctggaatga gtcatggaca gtgaagccat gtgagaggag aatgtcttca 1844
gagactccaa gggaaagcaa gcccactgccc tg 1876

<210> 7
<211> 422
<212> PRT
<213> Mus musculus

<400> 7

Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Asn Val Ala Pro Ala
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Thr Thr Thr Ala Thr Met Pro Leu Ala Pro Val Ala Pro Ala Asp Asn
20 25 30

Ser Thr Glu Ser Thr Gly Pro Gly Glu Ser Gln Glu Asp Met Phe Ala
35 40 45

Lys Leu Lys Glu Lys Phe Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro
50 55 60

Pro Trp Ala Leu Ile Ala Met Ala Val Val Ala Gly Leu Leu Leu Leu
65 70 75 80

Thr Cys Cys Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys
85 90 95

Asn Lys Lys Glu Lys Gly Lys Met Lys Asn Ala Met Asn Met Lys
100 105 110

Asp Met Lys Gly Gly Gln Asp Asp Asp Asp Ala Glu Thr Gly Leu Thr
115 120 125

Glu Gly Glu Gly Glu Gly Glu Glu Lys Glu Pro Glu Asn Leu Gly
130 135 140

Lys Leu Gln Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr
145 150 155 160

Val Gly Val Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly
165 170 175

Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys
180 185 190

Lys Tyr Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn
195 200 205

Glu Thr Phe Thr Phe Lys Val Pro Tyr Gln Glu Leu Ala Gly Lys Thr
210 215 220

Leu Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile
225 230 235 240

Ile Gly Glu Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro
245 250 255

Ile Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu
260 265 270

Lys Leu Gly Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly
275 280 285

Lys Leu Thr Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp
290 295 300

Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn
305 310 315 320

Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu
325 330 335

Asn Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln
340 345 350

Ile Gln Lys Val Gln Val Val Thr Val Leu Asp Tyr Asp Lys Leu
355 360 365

Gly Lys Asn Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr
370 375 380

Gly Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg
385 390 395 400

Pro Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu Glu Val Asp Ala
405 410 415

Leu Leu Gly Lys Asn Lys
420

<210> 8
<211> 2681
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (115)..(1383)

<220>
<221> misc_feature
<222> (232)..(294)
<223> BoNT/B binding domain

<220>
<221> misc_feature
<222> (295)..(375)
<223> Gangliosides binding domain or transmembrane domain

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ggtccccctct tcccactccc gcgcgcggcca gcgcgtgcggc tcccctctgc cacc atg 117
Met
1

aga aac atc ttc aag agg aac cag gag ccc att gtg gct ccg gcc acc 165
Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Ile Val Ala Pro Ala Thr
5 10 15

acc act gcc aca atg cct ctg gca ccc gcc gca cct gcc gat aac tct 213
Thr Thr Ala Thr Met Pro Leu Ala Pro Ala Ala Pro Ala Asp Asn Ser
20 25 30

aca gag agc acg ggc acc ggg gag agc caa gaa gac atg ttc gcc aag 261
Thr Glu Ser Thr Gly Thr Gly Glu Ser Gln Glu Asp Met Phe Ala Lys
35 40 45

ctg aag gac aaa ttc ttc aat gag atc aac aag atc cct ttg ccc ccc 309
Leu Lys Asp Lys Phe Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro Pro
50 55 60 65

tgg gct ctg att gcc atg gcc gtg gtt gct ggc ctc ctg ctg ctc acc 357

Trp Ala Leu Ile Ala Met Ala Val Val Ala Gly Leu Leu Leu Thr
70 75 80
tgc tgc ttc tgc atc tgt aag aag tgc tgc tgc aag aag aag aaa aac 405
Cys Cys Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Asn
85 90 95
aag aag gag aag ggc aaa ggc atg aag aac gcc atg aac atg aag gac 453
Lys Lys Glu Lys Gly Lys Gly Met Lys Asn Ala Met Asn Met Lys Asp
100 105 110
atg aag ggg ggc cag gat gat gac gac gcg gag aca ggc ctg act gaa 501
Met Lys Gly Gly Gln Asp Asp Asp Asp Ala Glu Thr Gly Leu Thr Glu
115 120 125
gga gaa gga gaa ggc gag gag gag aaa gag ccg gag aac ctg ggc aaa 549
Gly Glu Gly Glu Gly Glu Glu Glu Lys Glu Pro Glu Asn Leu Gly Lys
130 135 140 145
ttg cag ttt tct ctg gac tat gat ttc caa gcc aac cag ctc acc gtg 597
Leu Gln Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr Val
150 155 160
ggc gtc ctg cag gct gct gaa ctc ccg gcc ctg gac atg ggt ggc acg 645
Gly Val Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr
165 170 175
tca gac cct tac gtc aaa gtc ttc ctc ctc cca gac aag aag aag aaa 693
Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys
180 185 190
tat gag acc aag gtg cac ccg aag aca ctg aac cca gcc ttc aac gaa 741
Tyr Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn Glu
195 200 205
act ttc act ttc aag gtg cca tac cag gag tta gga ggc aaa acc ctg 789
Thr Phe Thr Phe Lys Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr Leu
210 215 220 225
gtg atg gct atc tat gac ttt gac cgc ttc tct aag cat gac atc atc 837
Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile
230 235 240
ggg gag gtg aaa gtg ccc atg aac acg gtg gac ctt ggc cag ccc atc 885
Gly Glu Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro Ile
245 250 255
gag gaa tgg aga gac cta caa ggc gga gag aag gaa gag cca gag aag 933
Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu Lys
260 265 270
ctg ggt gac atc tgt acc tcc ttg cgc tac gtg ccc act gct ggg aag 981
Leu Gly Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys
275 280 285
ctc acc gtc tgt atc ctg gag gcc aag aac ctg aag aag atg gat gtg 1029
Leu Thr Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val
290 295 300 305
ggg ggc ctc tca gac ccc tat gtg aag atc cac ttg atg cag aat ggc 1077
Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn Gly

	310	315	320	
aag aga ctc aag aag aag aac acg acg gtg aag aag aag acc ttg aac Lys Arg Leu Lys Lys Lys Thr Thr Val Lys Lys Thr Leu Asn	325	330	335	1125
ccc tac ttc aat gag tca ttc acg ttc gag atc ccc ttt gag cag atc Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln Ile	340	345	350	1173
cag aaa gtc cag gtc gtc acc gtg cta gac tat gac aaa ctg ggc Gln Lys Val Gln Val Val Thr Val Leu Asp Tyr Asp Lys Leu Gly	355	360	365	1221
aag aat gaa gcc atc gga aag atc ttc gta ggc acg aac gct aca ggc Lys Asn Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr Gly	370	375	380	1269
acg gag ctg cgg cac tgg tcc gac atg ctg gcg aac cct cgg agg ccc Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg Pro	390	395	400	1317
atc gcc cag tgg cac tct ctg aag cct gag gaa gaa gtg gat gct ctt Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu Val Asp Ala Leu	405	410	415	1365
ctg ggc aag aac aag tag gcagcggcgc ctggggccac gccccagagg Leu Gly Lys Asn Lys	420			1413
acactgacga gctccagagc tatcaataacc tcagttatgc gaccttagag gtttcttcat				1473
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tattgtccca ggagctgtcc ttgttgcatt ccctatcactg gttgccctc accccaagtg				1653
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gtggcaagca cattctgtgt ctgcactgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgt				1773
tgtgtgtgtg tgtgtgtgtc cacgtgtgcc catccatccc cacctgcct ctgtttggaa				1833
tatctcttcg tttctggaat gagtcacgga caatgatgcc gtgtgagaga ggaaagtctt				1893
caggtactcc gaggtgagga gagcccactg cttaagtggc cagaggccag aagctctcat				1953
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gaccgccagc tccaggatgt cattttgtt gacgacatca aactttgaag aaacagaagt				2193
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gcagagtaca agcagtgcgt tcatttgcatt tcacgcacca tctgcttttgc cctctgtttc				2313
cctttttgtg taagtggaaa aataccatct gacgataagt gctttgcaca gagccagaga				2373

cctattagag ggatgcttgg gtgttagtt cccttgaggc ccaggttaagg aggaggtgtc 2433
aagaagggga gcgttggtgg acagtgacaa gctagacatt gcagagctcc tcacaactcc 2493
tattcctgac cctctggacc ctttgacct cagtgtgg agccggagta gcccaggcag 2553
accttaggag aggccccgtc cttcccttcc ttagacagtt ttctcagaat gccaggaaac 2613
acagcgcat catttcagat gggtgttggaa gaaaatgtgc taaggttgc accctatgtt 2673
cggaattc 2681

<210> 9
<211> 422
<212> PRT
<213> Rattus norvegicus

<400> 9

Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Ile Val Ala Pro Ala
1 5 10 15

Thr Thr Thr Ala Thr Met Pro Leu Ala Pro Ala Ala Pro Ala Asp Asn
20 25 30

Ser Thr Glu Ser Thr Gly Thr Gly Glu Ser Gln Glu Asp Met Phe Ala
35 40 45

Lys Leu Lys Asp Lys Phe Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro
50 55 60

Pro Trp Ala Leu Ile Ala Met Ala Val Val Ala Gly Leu Leu Leu Leu
65 70 75 80

Thr Cys Cys Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys
85 90 95

Asn Lys Lys Glu Lys Gly Lys Met Lys Asn Ala Met Asn Met Lys
100 105 110

Asp Met Lys Gly Gly Gln Asp Asp Asp Asp Ala Glu Thr Gly Leu Thr
115 120 125

Glu Gly Glu Gly Glu Gly Glu Glu Lys Glu Pro Glu Asn Leu Gly
130 135 140

Lys Leu Gln Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr
145 150 155 160

Val Gly Val Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly
165 170 175

Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys
180 185 190

Lys Tyr Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn
195 200 205

Glu Thr Phe Thr Phe Lys Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr
210 215 220

Leu Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile
225 230 235 240

Ile Gly Glu Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro
245 250 255

Ile Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu
260 265 270

Lys Leu Gly Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly
275 280 285

Lys Leu Thr Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp
290 295 300

Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn
305 310 315 320

Gly Lys Arg Leu Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu
325 330 335

Asn Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln
340 345 350

Ile Gln Lys Val Gln Val Val Thr Val Leu Asp Tyr Asp Lys Leu
355 360 365

Gly Lys Asn Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr
370 375 380

Gly Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg
385 390 395 400

Pro Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu Val Asp Ala

405

410

415

Leu Leu Gly Lys Asn Lys
420

<210> 10
<211> 419
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (37)..(57)
<223> BoNT/B binding domain

<220>
<221> MISC_FEATURE
<222> (58)..(84)
<223> Gangliosides binding domain or transmembrane domain

<400> 10

Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Ile Val Ala Pro Ala
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Thr Thr Thr Ala Thr Met Pro Ile Gly Pro Val Asp Asn Ser Thr Glu
20 25 30

Ser Gly Gly Ala Gly Glu Ser Gln Glu Asp Met Phe Ala Lys Leu Lys
35 40 45

Glu Lys Leu Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro Pro Trp Ala
50 55 60

Leu Ile Ala Ile Ala Val Val Ala Gly Leu Leu Leu Thr Cys Cys
65 70 75 80

Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys Asn Lys Lys
85 90 95

Glu Lys Gly Lys Gly Met Lys Asn Ala Met Asn Met Lys Asp Met Lys
100 105 110

Gly Gly Gln Asp Asp Asp Ala Glu Thr Gly Leu Thr Glu Gly Glu
115 120 125

Gly Glu Gly Glu Glu Lys Glu Pro Glu Asn Leu Gly Lys Leu Gln
130 135 140

Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr Val Gly Val
145 150 155 160

Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp
165 170 175

Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Tyr Glu
180 185 190

Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn Glu Thr Phe
195 200 205

Thr Phe Lys Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr Leu Val Met
210 215 220

Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu
225 230 235 240

Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro Ile Glu Glu
245 250 255

Trp Arg Asp Leu Gln Gly Glu Lys Glu Glu Pro Glu Lys Leu Gly
260 265 270

Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys Leu Thr
275 280 285

Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val Gly Gly
290 295 300

Leu Ser Asp Pro Tyr Gly Lys Ile His Leu Met Gln Asn Gly Lys Arg
305 310 315 320

Leu Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu Asn Pro Tyr
325 330 335

Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln Ile Gln Lys
340 345 350

Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Leu Gly Lys Asn
355 360 365

Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr Gly Thr Glu
370 375 380

Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg Pro Ile Ala

385

390

395

400

Gln Trp His Ser Leu Lys Pro Glu Glu Val Asp Ala Leu Leu Gly
405 410 415

Lys Asn Lys